

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: THE SCRIPPS RESEARCH INSTITUTE
- (B) STREET: 10550 North Torrey Pines Road
- (C) CITY: La Jolla
- (D) STATE: California
- (E) COUNTRY: US
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(ii) TITLE OF INVENTION: MHC CLASS II ANTIGEN PRESENTING SYSTEMS
AND METHODS FOR ACTIVATING CD4+ T CELLS

(iii) NUMBER OF SEQUENCES: 56

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(v) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US97/
- (B) FILING DATE: 22-MAY-1997
- (C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 60/018,175
- (B) FILING DATE: 23-MAY-1996

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

09746256.1.1.00

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATTTCGATGCA CACTCACATT CTTCTCCTAA TACGATAATA AAACCTTTCCA TGAAAAATAT	60
GGAAAAATAT ATGAAAATTG AGAAATCCAA AAAACTGATA AACGCTCTAC TTAATTAAAA	120
TAGATAAATG GGAGCGGCTG GAATGGCGGA GCATGACCAA GTTCCTCCGC CAATCAGTCG	180
TAAAACAGAA GTCGTGGAAG GCGGATAGAA AGAATGTTCC ATTTGACGGG CAAGCATGTC	240
TGCTATGTGG CGGATTGCGG AGGAATTGCA CTGGAGACCA GCAAGGTTCT CATGACCAAG	300
AATATAGCGG TGTGAGTGAG CGGGAAGCTC GGTTCCTGTC CAGATCGAAC TCAAAACTAG	360
TCCAGCCAGT CGCTGTCGAA ACTAATTAAG TTAATGAGTT TTTCATGTGA GTTTCGCGCT	420
GAGCAACAAT TAAGTTTATG TTTCAGTTCG GCTTAGATTT CGCTGAAGGA CTTGCCACTT	480
TCAATCAATA CTTTAGAACA AAATCAAAAC TCATTCTAAT AGCTTGGTGT TCATCTTTT	540
TTTTAATGAT AAGCATTTTG TCGTTTATAC TTTTATATT TCGATATTAA ACCACCTATG	600
AAGTTCATTT TAATCGCCAG ATAAGCAATA TATTGTGTA ATATTTGTAT TCTTTATCAG	660
GAAATTCAGG GAGACGGGGA AGTTACTATC TACTAAAAGC GAAACAATTT CTTACAGTTT	720
TACTCTCTCT ACTCTAGAGT	740

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATTCGTTGC AGGACAGGAT GTGGTGCCCG ATGTGACTAG CTCTTTGCTG CAGGCCGTCC	60
TATCCTCTGG TTCCGATAAG AGACCCAGAA CTCCGGCCCC CCACCGCCCA CCGCCACCCC	120

CATACATATG TGGTACGCAA GTAAGAGTGC CTGCGCATGC CCCATGTGCC CCACCAAGAG 180
TTTTGCATCC CATACAAGTC CCCAAAGTGG AGAACCGAAC CAATTCTTGG CGGGCAGAAC 240
AAAAGCTTCT GCACACGTCT CCACTCGAAT TTGAGCCGG CCGGCGTGTG CAAAAGAGGT 300
GAATCGAACG AAAGACCCGT GTGTAAAGCC GCGTTTCAA AATGTATAAA ACCGAGAGCA 360
TCTGGCCAAT GTGCATCAGT TGTGGTCAGC AGCAAAATCA AGTGAATCAT CTCAGTGCAA 420
CTAAAGG 427

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTGAATTCC ACCATGCCGT GCAGCAGAGC TCTGA 35

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTGGATCCT CATAAAGGCC CTGGGTGTC 29

09745091 44700

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTTGAATTCC ACCATGGCTC TGCAGATCCC CA

32

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTGGATCCT CACTGCAGGA GCCCTGCT

28

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4713 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GC GTTGCAGG ACAGGATGTG GTGCCC GATG TGA CTAGCTC TTTGCTGCAG GCCGTCTTAT	60
CCTCTGGTTC CGATAAGAGA CCCAGAACTC CGGCCCCCCA CCGCCCACCG CCACCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCCTG CGCATGCCCC ATGTGCCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGCGG GCAGAACAAA	240
AGTTTCTGCA CACGTCTCCA CTCGAATTTG GAGCCGGCCG GCGTGTGCAA AAGAGGTGAA	300
TCGAACGAAA GACCCGTGTG TAAAGCCCGG TTTCCAAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTCA GCAGC AAAATCAAGT GAATCATCTC AGTGCAACTA	420
AAGGGGGGAA TTCCTGCAGA GACCTCCCAG AGACCAGGAT GCCGTGCAGC AGAGCTCTGA	480
TTCTGGGGGT CCTCGCCCTG AACACCATGC TCAGCCTCTG CGGAGGTGAA GACGACATTG	540
AGGCCGACCA CGTAGGCTTC TATGGTACAA CTGTTTATCA GTCTCCTGGA GACATTGGCC	600
AGTACACACA TGAATTTGAT GGTGATGAGT TGTCTATGT GGA CTTGAT AAGAAGAAAA	660
CTGTCTGGAG GCTTCCTGAG TTTGGCCAAT TGATACTCTT TGAGCCCCAA GGTGGACTGC	720
AAAACATAGC TGCAGAAAAA CACA ACTTGG GAATCTTGAC TAAGAGGTCA AATTTACCC	780
CAGCTACCAA TGAGGCTCCT CAAGCGACTG TGTCCCCAA GTCCCTGTG CTGCTGGGTC	840
AGCCCAACAC CTTATCTGC TTTGTGGACA ACATCTTCCC ACCTGTGATC AACATCACAT	900
GGCTCAGGAA TAGCAAGTCA GTCACAGACG GCGTTTATGA GACGAGCTTC CTCGTCAACC	960
GTGACCATTC CTTCCACAAG CTGTCTTATC TCACCTTCAT CCCTTCTGAT GATGACATTT	1020
ATGACTGCAA GGTGGAGCAC TGGGGCCTGG AGGAGCCGGT TCTGAAACAC TGGGAACCTG	1080
AGATTCCAGC CCCCATGTCA GAGCTGACAG AAAGTGTGCT GTGTGCCCTG GGGTTGTCTG	1140
TGGGCCTTGT GGGCATCGTG GTGGGCACCA TCTTCATCAT TCAAGGCCTG CGATCAGGTG	1200
GCACCTCCAG ACACCCAGGG CCTTTATGAG TCACACCCTG GAAAGGAAGG TGTGTGTCCC	1260
TCTTCATGGA AGAAGTGGTG TTCTGGGTGT CGAATTCGAG CTCGGTACCC GGGGATCCTC	1320
TAGAGTCGAC CTGCAGGCAT GCAATTCGAT GCACACTCAC ATTCTTCTCC TAATACGATA	1380
ATAAACTTT CCATGAAAAA TATGAAAAA TATATGAAAA TTGAGAAATC CAAAAA CTG	1440
ATAAACGCTC TACTTAATTA AAATAGATAA ATGGGAGCGG CAGGAATGGC GGAGCATGGC	1500
CAAGTTCCTC CGCCAATCAG TCGTAAACA GAAGTCGTGG AAAGCGGATA GAAAGAAATGT	1560
TGCAATTTGAC GGGCAAGCAT GTCTGCTATG TGGCGGATTG CGGAGGAATT GCACTGGAGA	1620
CCAGCAAGGT TCTCATGACC AAGAATATAG CGGTGAGTGA GCGGGAAGCT CGGTTTCTGT	1680
CCAGATCGAA CTCAAAACTA GTCCAGCCAG TCGCTGTCTGA AACTAATTAA GTAAATGAGT	1740

TTTTCATGTT	AGTTTCGCGC	TGAGCAACAA	TTAAGTTTAT	GTTTCAGTTC	GGCTTAGATT	1800
TGCCTGAAGG	ACTTGCCACT	TTCAATCAAT	ACTTTAGAAC	AAAATCAAAA	CTCATTCTAA	1860
TAGCTTGGTG	TTCATCTTTT	TTTTTAATGA	TAAGCATTTT	GTCGTTTATA	CTTTTATAT	1920
TTCGATATTA	AACCACCTAT	GAAGTTCATT	TTAATCGCCA	GATAAGCAAT	ATATTGTGTA	1980
AATATTTGTA	TTCTTTATCA	GGAAATTCAG	GGAGACGGGG	AAGTTACTAT	CTACTAAAAG	2040
CCAAACAATT	TCTTACAGTT	TTACTCTCTC	TACTCTAGAG	CTTGGCACTG	GCCGTCGTTT	2100
TACAACGTCG	TGACTGGGAA	AACCCTGGCG	TTACCCAAC	TAATCGCCTT	GCAGCACATC	2160
CCCCTTTCGC	CAGCTGGCGT	AATAGCGAAG	AGGCCCGCAC	CGATCGCCCT	TCCCAACAGT	2220
TGGCGAGCCT	GAATGGCGAA	TGGCGCCTGA	TGCGGTATTT	TCTCCTTACG	CATCTGTGCG	2280
GTATTTTACA	CCGCATATGG	TGCACTCTCA	GTACAATCTG	CTCTGATGCC	GCATAGTTAA	2340
GCCAGCCCCG	ACACCCGCCA	ACACCCGCTG	ACGCGCCCTG	ACGGGCTTGT	CTGCTCCCGG	2400
CATCCGCTTA	CAGACAAGCT	GTGACCGTCT	CCGGGAGCTG	CATGTGTCAG	AGGTTTTCAC	2460
CGTCATCACC	GAAACGCGCG	AGACGAAAGG	GCCTCGTGAT	ACGCCTATTT	TTATAGGTAA	2520
ATGTCATGAT	AATAATGGTT	TCTTAGACGT	CAGGTGGCAC	TTTTCGGGGA	AATGTGCGCG	2580
GAACCCCTAT	TTGTTTATTT	TTCTAAATAC	ATTCAAATAT	GTATCCGCTC	ATGAGACAAT	2640
AACCCTGATA	AATGCTTCAA	TAATATTGAA	AAAGGAAGAG	TATGAGTATT	CAACATTTCC	2700
GTGTCGCCCT	TATTCGCTTT	TTTGCGGCAT	TTTGCCTTCC	TGTTTTTGCT	CACCCAGAAA	2760
CGCTGGTGAA	AGTAAAAGAT	GCTGAAGATC	AGTTGGGTGC	ACGAGTGGGT	TACATCGAAC	2820
TGGATCTCAA	CAGCGGTAAG	ATCCTTGAGA	GTTTTCGCCC	CGAAGAACGT	TTTCCAATGA	2880
TGAGCACTTT	TAAAGTTCTG	CTATGTGGCG	CGGTATTATC	CCGTATTGAC	GCCGGGCAAG	2940
AGCAACTCGG	TCGCCGCATA	CACTATTCTC	AGAATGACTT	GGTTGAGTAC	TCACCAGTCA	3000
CAGAAAAGCA	TCTTACGGAT	GGCATGACAG	TAAGAGAATT	ATGCAGTGCT	GCCATAACCA	3060
TGAGTGATAA	CACTGCGGCC	AACTTACTTC	TGACAACGAT	CGGAGGACCG	AAGGAGCTAA	3120
CCGCTTTTTT	GCACAACATG	GGGGATCATG	TAAGTGCCTT	TGATCGTTGG	GAACCGGAGC	3180
TGAATGAAGC	CATACCAAAC	GACGAGCGTG	ACACCACGAT	GCCTGTAGCA	ATGGCAACAA	3240
CGTTGCGCAA	ACTATTAACT	GGCGAACTAC	TTACTCTAGC	TTCCCGGCAA	CAATTAATAG	3300
ACTGGATGGA	GGCGGATAAA	GTTGCAGGAC	CACTTCTGCG	CTCGGCCCTT	CCGGCTGGCT	3360
GGTTTATTGC	TGATAAATCT	GGAGCCGGTG	AGCGTGGGTC	TCGCGGTATC	ATTGCAGCAC	3420
TGGGGCCAGA	TGGTAAGCCC	TCCCGTATCG	TAGTTATCTA	CACGACGGGG	AGTCAGGCAA	3480
CTATGGATGA	ACGAAATAGA	CAGATCGCTG	AGATAGGTGC	CTCACTGATT	AAGCATTGGT	3540
AACTGTCAGA	CCAAGTTTAC	TCATATATAC	TTTAGATTGA	TTTAAAACTT	CATTTTTAAT	3600
TTAAAAGGAT	CTAGGTGAAG	ATCCTTTTTG	ATAATCTCAT	GACCAAAATC	CCTTAACGTG	3660
AGTTTTTCGT	CCACTGAGCG	TCAGACCCCG	TAGAAAAGAT	CAAAGGATCT	TCTTGAGATC	3720
CTTTTTTTCT	GCGCGTAATC	TGCTGCTTGC	AAACAAAAAA	ACCACCGCTA	CCAGCGGTGG	3780
TTTGTTTGCC	GGATCAAGAG	CTACCAACTC	TTTTTCCGAA	GGTAACTGGC	TTCAGCAGAG	3840
CGCAGATACC	AAATACTGTC	CTTCTAGTGT	AGCCGTAGTT	AGGCCACCAC	TTCAAGAACT	3900
CTGTAGCACC	GCCTACATAC	CTCGCTCTGC	TAATCCTGTT	ACCAGTGGCT	GCTGCCAGTG	3960
GCGATAAGTC	GTGTCTTACC	GGGTTGGACT	CAAGACGATA	GTTACCGGAT	AAGGCGCAGC	4020
GGTCGGGCTG	AACGGGGGGT	TCGTGCACAC	AGCCCAGCTT	GGAGCGAACG	ACCTACACCG	4080

AACTGAGATA CCTACAGCGT GAGCATTGAG AAAGCGCCAC GCTTCCCGAA GGGAGAAAGG 4140
CGGACAGGTA TCCGTAAGC GGCAGGGTCG GAACAGGAGA GCGCACGAGG GAGCTTCCAG 4200
GGGGAAACGC CTGGTATCTT TATAGTCCTG TCGGGTTTCG CCACCTCTGA CTTGAGCGTC 4260
GATTTTTGTG ATGCTCGTCA GGGGGGCGGA GCCTATGGAA AAACGCCAGC AACCGGGCCT 4320
TTTTACGGTT CCTGGCCTTT TGCTGGCCTT TTGCTCACAT GTTCTTTCCT GCGTTATCCC 4380
CTGATTCTGT GGATAACCGT ATTACCGCCT TTGAGTGAGC TGATACCGCT CGCCGCAGCC 4440
GAACGACCGA GCGCAGCGAG TCAGTGAGCG AGGAAGCGGA AGAGCGCCCA ATACGCAAAC 4500
CGCCTCTCCC CGCGCGTTGG CCGATTCAAT AATGCAGCTG GCACGACAGG TTTCCCGACT 4560
GGAAAGCGGG CAGTGAGCGC AACGCAATTA ATGTGAGTTA GCTCACTCAT TAGGCACCCC 4620
AGGCTTTACA CTTTATGCTT CCGGCTCGTA TGTGTGTGG AATTGTGAGC GGATAACAAT 4680
TTCACACAGG AAACAGCTAT GACCATGATT ACG 4713

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4724 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGTTGCAGG ACAGGATGTG GTGCCCGATG TGA TAGCTC TTTGCTGCAG GCCGTCCTAT 60
CCTCTGGTTC CGATAAGAGA CCGAGAACTC GGGCCCCCA CCGCCACCG CCACCCCAT 120
ACATATGTGG TACGCAAGTA AGAGTGCCGTG CGCATGCCCC ATGTGCCCCA CCAAGAGTTT 180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGCGG GCAGAACAAA 240
AGCTTCTGCA CACGTCTCCA CTCGAATTTG GAGCCGGCCG GCCTGTGCAA AAGAGGTGAA 300
TCGAACGAAA GACCCGTGTG TAAAGCCGCG TTTCCAAAAT GTATAAAACC GAGAGCATCT 360
GGCCAATGTG CATCAGTTGT GGTGAGCAGC AAAATCAAGT GAATCATCTC AGTGCAACTA 420
AAGGGGGGAA TTCCCTGCTG TGCCCTAGAG ATGGCTCTGC AGATCCCCAG CCTCCTCCTC 480
TCAGCTGCTG TGGTGGTGCT GATGGTGCTG AGCAGCCAG GGA CTGAGGG CGGAAACTCC 540
GAAAGGCATT TCGTGGTCCA GTTCAAGGGC GAGTGCTACT ACACCAACGG GACGCAGCGC 600
ATACGGCTCG TGACCAGATA CATCTACAAC CGGGAGGAGT ACGTGCGCTA CGACAGCGAC 660
GTGGGCGAGT ACCGCGCGGT GACCGAGCTG GGGCGGCCAG ACGCCGAGTA CTGGAACAGC 720

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CAGCCGGAGA TCCTGGAGCG AACCGGGGCC GAGGTGGACA CGGCGTGCAG ACACAACCTAC 780
GAGGGGGCCG AGACCAGCAC CTCCCTGCGG CGGCTTGAAC AGCCCAATAT CGCCATCTCC 840
CTGTCCAGGA CAGAGGCCCT CAACCACCAC AACACTCTGG TCTGTTCCGT GACAGATTTT 900
TACCCAGCCA AGATCAAAGT GCGCTGGTTC AGGAATGGCC AGGAGGAGAC AGTGGGGGTC 960
TCATCCACAC AGCTTATTAG GAATGGGGAC TGGACCTTCC AGGTCCTGGT CATGCTGGAG 1020
ATGACCCCTC ATCAGGGAGA GGTCTACACC TGCCATGTGG AGCATCCCAG CCTGAAGAGC 1080
CCCATCACTG TGGAGTGGAG GGCACAGTCC GAGTCTGCCC GGAGCAAGAT GTTGAGCGGC 1140
ATCGGGGGCT GCGTGCTTGG GGTGATCTTC CTCGGGCTCG GCCTTTTCAT CCGTCACAGG 1200
AGTCAGAAAG GACCTCGAGG CCCTCCTCCA GCAGGGCTCC TGCAGTGA CTGAGTGT 1260
TGA CTGAGT GACTGTCTCA GACTGTAAGA CCTACATGTC TCGAATTCGA GCTCGGTACC 1320
CGGGGATCCT CTAGAGTCGA CCTGCAGGCA TGCAATTCGA TGCACACTCA CATTCTTCTC 1380
CTAATACGAT AATAAACTT TCCATGAAAA ATATGAAAA ATATATGAAA ATTGAGAAAT 1440
CCAAAAACT GATAAACGCT CTACTTAATT AAAATAGATA AATGGGAGCG GCAGGAATGG 1500
CGGAGCATGG CCAAGTTTCT CCGCCAATCA GTCGTAAAC AGAAGTCGTG GAAAGCGGAT 1560
AGAAAGAATG TTCGATTGA CGGGCAAGCA TGTCTGCTAT GTGGCGGATT GCGGAGGAAT 1620
TGCACTGGAG ACCAGCAAGG TTCTCATGAC CAAGAATATA GCGGTGAGTG AGCGGGAAGC 1680
TCGGTTTCTG TCCAGATCGA ACTCAAACT AGTCCAGCCA GTCGCTGTCTG AAATAATTA 1740
AGTAAATGAG TTTTTCATGT TAGTTTCGCG CTGAGCAACA ATTAAGTTTA TGTTCAGTT 1800
CGGCTTAGAT TTCGCTGAAG GACTTGCCAC TTTCAATCAA TACTTTAGAA CAAAAACAA 1860
ACTCATTCTA ATAGCTTGGT GTTCATCTTT TTTTAAATG ATAAGCATTT TGTGCTTTAT 1920
ACTTTTTATA TTTCCGATATT AAACCACCTA TGAAGTTTCT TTTAATCGCC AGATAAGCAA 1980
TATATTGTGT AAATATTTGT ATTCTTTATC AGGAAATTCA GGGAGACGGG GAAGTTACTA 2040
TCTACTAAAA GCCAAACAAT TTCTTACAGT TTTACTCTCT CTACTCTAGA GCTTGGCACT 2100
GGCGTCTGTT TTACAACGTC GTGACTGGGA AAACCCTGGC GTTACCCAAC TTAATCGCCT 2160
TGCAGCACAT CCCCCTTTCG CCAGCTGGCG TAATAGCGAA GAGGCCCGCA CCGATCGCCC 2220
TTCCCAACAG TTGCGCAGCC TGAATGGCGA ATGGCGCCTG ATGCGGTATT TTCTCCTTAC 2280
GCATCTGTGC GGTATTTAC ACCGCATATG GTGCACTCTC AGTACAATCT GCTCTGATGC 2340
CGCATACTTA AGCCAGCCCC GACACCCGCC AACACCCGCT GACGCGCCCT GACGGGCTTG 2400
TCTGCTCCCG GCATCCGCTT ACAGACAAGC TGTGACCGTC TCCGGGAGCT GCATGTGTCA 2460
GAGGTTTTCA CCGTCATCAC CGAAACGCGC GAGACGAAAG GGCCTCGTGA TACGCCTATT 2520
TTTATAGGTT AATGTCATGA TAATAATGGT TTCTTAGACG TCAGGTGGCA CTTTTCGGGG 2580
AAATGTGCGC GGAACCCCTA TTTGTTTATT TTTCTAAATA CATTCAAATA TGTATCGGCT 2640
CATGAGACAA TAACCCTGAT AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT 2700
TCAACATTTT CGTGTCGCCC TTATTCCCTT TTTTGCGGCA TTTTGCCCTC CTGTTTTTGC 2760
TCACCCAGAA ACGCTGGTGA AAGTAAAAGA TGCTGAAGAT CAGTTGGGTG CACGAGTGGG 2820
TTACATCGAA CTGGATCTCA ACAGCGGTAA GATCCTTGAG AGTTTTCGCC CCGAAGAACG 2880
TTTTCCAATG ATGAGCACTT TTAAAGTTCT GCTATGTGGC GCGGTATTAT CCCGTATTGA 2940
CGCCGGGCAA GAGCAACTCG GTCGCCGCAT AACTATTCT CAGAATGACT TGTTGAGTA 3000
CTCACCAGTC ACAGAAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAT TATGCAGTGC 3060

TGCCATAACC	ATGAGTGATA	ACACTGCCGC	CAACTTACTT	CTGACAACGA	TCGGAGGACC	3120
GAAGGAGCTA	ACCGCTTTTT	TGCACAACAT	GGGGGATCAT	GTAACGCGCC	TTGATCGTTG	3180
GGAACCGGAG	CTGAATGAAG	CCATACCAAA	CGACGAGCGT	GACACCACGA	TGCCTGTAGC	3240
AATGGCAACA	ACGTTGCGCA	AACTATTAAC	TGGCGAACTA	CTTACTCTAG	CTTCCCGGCA	3300
ACAATTAATA	GA CTGGATGG	AGGCGGATAA	AGTTGCAGGA	CCACTTCTGC	GCTCGGCCCT	3360
TCCGGCTGGC	TGGTTTATTG	CTGATAAATC	TGGAGCCGGT	GAGCGTGGGT	CTCGCGGTAT	3420
CATTGCAGCA	CTGGGGCCAG	ATGGTAAGCC	CTCCCGTATC	G TAGTTATCT	ACAGGACGGG	3480
GAGTCAGGCA	ACTATGGATG	AACGAAATAG	ACAGATCGCT	GAGATAGGTG	CCTCACTGAT	3540
TAAGCATTGG	TA ACTGTCAG	ACCAAGTTA	CTCATATATA	CTTTAGATTG	ATTTAAAACT	3600
TCATTTTAA	TTTAAAAGGA	TCTAGGTGAA	GATCCTTTTT	GATAATCTCA	TGACCAAAAT	3660
CCCTTAACGT	GAGTTTTTCGT	TCCACTGAGC	GTCAGACCCC	G TAGAAAAGA	TCAAAGGATC	3720
TTCTTGAGAT	CCTTTTTTTC	TGCGCGTAAT	CTGCTGCTTG	CAAACAAAAA	AACCACCGCT	3780
ACCAGCGGTG	GTTTGTTTGC	CGGATCAAGA	GCTACCAACT	CTTTTTCCGA	AGGTA ACTGG	3840
CTTCAGCAGA	GCGCAGATAC	CAAATACTGT	CCTTCTAGTG	TAGCCGTACT	TAGGCCACCA	3900
CTTCAAGAAC	TCTGTAGCAC	CGCCTACATA	CCTCGCTCTG	CTAATCCTGT	TACCACTGGC	3960
TGCTGCCAGT	GCGGATAAGT	CGTGTCTTAC	CGGGTTGGAC	TCAAGACGAT	AGTTACCGGA	4020
TAAGGCGCAG	CGGTGCGGCT	GAACGGGGGG	TTCGTGCACA	CAGCCCAGCT	TGGAGCGAAC	4080
GACCTACACC	GAACTGAGAT	ACCTACAGCG	TGAGCATTGA	GAAAGCGCCA	CGCTTCCCGA	4140
AGGGAGAAAG	GCGGACAGGT	ATCCGGTAAG	CGGCAGGGTC	GGAACAGGAG	AGCGCACGAG	4200
GGAGCTTCCA	GGGGGAAACG	CCTGGTATCT	TTATAGTCCT	GTGCGGTTTC	GCCACCTCTG	4260
ACTTGAGCGT	CGATTTTTGT	GATGCTCGTC	AGGGGGGCGG	AGCCTATGGA	AAAACGCCAG	4320
CAACGCGGCC	TTTTTACGGT	TCCTGGCCTT	TTGCTGGCCT	TTTGCTCACA	TGTTCTTTCC	4380
TGCGTTATCC	CCTGATTCTG	TGGATAACCG	TATTACCGCC	TTTGAGTGAG	CTGATACCGC	4440
TCGCGCGCAG	CGAACGACCG	AGCGCAGCGA	GTCAGTGAGC	GAGGAAGCGG	AAGAGCGCCC	4500
AATACGCAAA	CGGCCTCTCC	CGCGCGTTG	GCCGATTCAT	TAATGCAGCT	GGCAGGACAG	4560
GTTTCCCGAC	TGGAAAGCGG	GCAGTGAGCG	CAACGCAATT	AATGTGAGTT	AGCTCACTCA	4620
TTAGGCACCC	CAGGCTTTAC	ACTTTATGCT	TCCGGCTCGT	ATGTTGTGTG	GAATTGTGAG	4680
CGGATAACAA	TTTCACACAG	GAAACAGCTA	TGACCATGAT	TACG		4724

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCACCATGGC CATTAGTGGA GTC

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTGGATCCT TACAGAGGCC CCCTGCGTT

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCACCATGGT GTGTCTGAGG CTCC

24

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGGATCCT CAGCTCAGGA ATCCTCTTG

29

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCACCATGGT CCTAAACAAA GCTCTGAT

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTGGATCCT CACAAGGGCC CTGGTGTCT

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCACCATGGC TTGAAGAAG GCCTTT

26

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTTAGATCTC AGTGCAGAAG CCCTTT

26

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CCACCATGGG CCCTGAAGAC AGAAT

25

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTGGATCCT CACAGGGTCC CCTGGGC

27

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCACCATGGT TCTGCAGGTT TCTGCG

26

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTGGATCCT TATGCAGATC CTCGTTGAA

29

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGAATTCAC TAGAGGCTAG AGCCAT

26

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AAGGATCCTC ACAGGGTGAC TTGACC

26

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2580 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGGTTGCAGG ACAGGATGTG GTGCCCCGATG TGACTAGCTC TTTGCTGCAG GCCGTCCTAT	60
CCTCTGGTTC CGATAAGAGA CCCAGAACTC CGGCCCCCCA CCGCCCACCG CCACCCCCAT	120
ACATATGTGG TACGCAAGTA AGAGTGCCTG CGCATGCCCC ATGTGCCCCA CCAAGAGTTT	180
TGCATCCCAT ACAAGTCCCC AAAGTGGAGA ACCGAACCAA TTCTTCGGG GCAGAACAAA	240
AGCTTCTGCA CAGTCTCCA CTCGAATTG GAGCCGGCCG GCGTGTGCAA AAGAGGTGAA	300
TCGAACGAAA GACCCGTGTG TAAAGCCGCG TTTCCAAAAT GTATAAAACC GAGAGCATCT	360
GGCCAATGTG CATCAGTTGT GGTGAGCAGC AAAATCAAGT GAATCATCTC AGTGCAACTA	420
AAGGGGGGAA TTCGATCTAG AGGCTAGAGC CATGGATGAC CAACGCGACC TCATCTCTAA	480
CCATGAGCAA TTGCCATAC TGGGCAACCG CCTAGAGAG CCAGAAAGGT GCAGCCGTGG	540
AGCTCTGTAC ACCGGTGTTC CTGTCTGGT GGCTCTGCTC TTGGCTGGGC AGGCCACCAC	600
TGCTTACTTC CTGTACCAGC AACAGGGCCG CCTAGACAAG CTGACCATCA CCTCCCAGAA	660
CCTGCAACTG GAGAGCCTTC GCATGAAGCT TCCGAAATCT GCCAAACCTG TGAGCCAGAT	720
GCGGATGGCT ACTCCCTTGC TGATGCGTCC AATGTCCATG GATAACATGC TCCTTGGGCC	780
TGTGAAGAAC GTTACCAAGT ACGGCAACAT GACCCAGGAC CATGTGATGC ATCTGCTCAC	840
GAGGTCTGGA CCCCTGGAGT ACCCGCAGCT GAAGGGGACC TTCCCAGAGA ATCTGAAGCA	900
TCTTAAGAAC TCCATGGATG GCGTGAAGT GAAGATCTTC GAGAGCTGGA TGAAGCAGTG	960
GCTCTTGTTC GAGATGAGCA AGAACTCCCT GGAGGAGAAG AAGCCCACAG AGGCTCCACC	1020
TAAAGAGCCA CTGGACATGG AAGACCTATC TTCTGGCCTG GGAGTGACCA GGCAGGAAGT	1080
GGGTCAAGTC ACCCTGTGAA GACAGAGGCC AGCATCAAGC TTATCGATAC CGTCGACCTG	1140
CAGGCATGCA ATTTCATGCA CACTCACATT CTCTCCTAA TACGATAATA AAACCTTCCA	1200
TGAAAAATAT GAAAAAATAT ATGAAAATTG AGAAATCCAA AAAACTGATA AACGCTCTAC	1260
TTAATTAAAA TAGATAAATG GGAGCGGCAG GAATGGCGGA GCATGGCCAA GTTCCTCCGC	1320
CAATCAGTCG TAAACAGAA CTCGTGGAAG GCGGATAGAA AGAATGTTG ATTTGACGGG	1380
CAAGCATGTC TGCTATGTGG CGGATTGCGG AGGAATTGCA CTGGAGACCA GCAAGTTTCT	1440
CATGACCAAG AATATAGCGG TGAGTGAGCG GGAAGCTCGG TTTCTGTCCA GATCGAACTC	1500
AAAACAGTC CAGCCAGTCG CTGTGGAAC TAATTAAGTA AATGAGTTT TCATGTTAGT	1560
TTGCGCTGA GCAACAATTA AGTTTATGTT TCAGTTCGGC TTAGATTTCG CTGAAGGACT	1620
TGCCACTTTC AATCAATACT TTAGAACAAA ATCAAACTC ATTCTAATAG CTTGGTGTTC	1680
ATCTTTTTTT TTAATGATAA GCATTTTGTG GTTTATACTT TTTATATTTC GATATTAAAC	1740
CACCTATGAA GTTCATTTTA ATCGCCAGAT AAGCAATATA TTGTGTAAAT ATTTGTATTC	1800
TTTATCAGGA AATTGAGGA GACGGGGAAG TTACTATCTA CTAAAAGCCA AACAATTTCT	1860
TACAGTTTTC CTCTCTCTAC TCTAGAGCTT GGCACTGGCC GTCGTTTTAC AACGTCGTGA	1920
CTGGGAAAAC CCTGGCGTTA CCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG	1980
CTGGCGTAAT AGCGAAGAGG CCGGCACCGA TCGCCCTTCC CAACAGTTGC GCAGCCTGAA	2040
TGGCGAATGG CGCCTGATGC GGTATTTTCT CCTTACGCAT CTGTGCGGTA TTTCACACCG	2100

CATATGGTGC	ACTCTCAGTA	CAATCTGCTC	TGATGCCGCA	TAGTTAAGCC	AGCCCCGACA	2160
CCCGCCAACA	CCCGCTGACG	CGCCCTGACG	GGCTTGTCTG	CTCCCGGCAT	CCGCTTACAG	2220
ACAAGCTGTG	ACCGTCTCCG	GGAGCTGCAT	GTGTCAGAGG	TTTTCACCGT	CATCACCGAA	2280
ACGCGCGAGA	CGAAAGGGCC	TCGTGATACG	CCTATTTTTA	TAGGTTAATG	TCATGATAAT	2340
AATGGTTTCT	TAGACGTCAG	GTGGCACTTT	TCGGGGAAAT	GTGCGCGGAA	CCCCTATTTG	2400
TTTATTTTTC	TAAATACATT	CAAATATGTA	TCCGCTCATG	AGACAATAAC	CCTGATAAAT	2460
GCTTCAATAA	TATTGAAAAA	GGAAGAGTAT	GAGTATTCAA	CATTTCGGTG	TCGCCCTTAT	2520
TCCCTTTTTT	GCGGCATTTT	GCCTTCCTGT	TTTGCTCAC	CCAGAAACGC	TGGTGAAAGT	2580

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AAGAATTCAC CATGGATGAT CAGCGCGACC TT

32

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAAGGATCCT CACATGGGGA CTGGGCCAG A

31

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACCATGGG TCATGAACAG AACCA

25

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTTGTCGACT CAGTCACCTG AGCAAGG

27

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAACCATGGT CTCATTCCTG CC

22

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTGTGACC TAGGAAATGT GCCATCC

27

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTTAGAATTC ACCATGGCTT CAACCCGTGC CAAG

34

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTAGTCGAC TCAGGGAGGT GGGGCTTGTC C

31

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

09715091-1-1700

ACCCTTGAAT TCATGGCTCC CAGCAGCCCC CGGCCC

36

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATTACCGGAT CCTCAGGGAG GCGTGGCTTG TGTGTTCCG

39

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAGGTACCCG TGGAGACTGC CAGAGAT

27

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TTTGATCCC TATGGCCGA AGGCCTG

27

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAGAATTCCT GTCAGAATGG CCACCAT

27

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TTTAGATCTT CACTCAGCTC TGGACGGT

28

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ACCCTTGAGC TCATGGTTGC TGGGAGCGAC GCGGGG

36

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

ATTACGGGAT CCTTAAAGAA CATTGATATA CAGCACAATA CA

42

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TTTAGAATTC ACCATGGCTT GCAATTGTCA GTTG

34

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TTTAGTCGAC CTAAAGGAAG ACGGTCTGTT C

31

(2) INFORMATION FOR SEQ ID NO:42:

09746256 PCT/US97/08697

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACCCTTGAAT CCATGGGCCA CACACGGAGG CAG

33

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ATTACCGGAT CCTTATACAG GCGGTACACT TTCCTTCT

39

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTTAGAATTG ACCATGGACC CCAGATGCAC CATGGG

36

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTTAGTCGAC TCACTCTGCA TTTGGTTTTG CTGA

34

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACCCTTGAGC TCATGGATCC CCAGTGCACT ATG

33

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ATTACCCCCG GGTAAAAAC ATGTATCACT TTTGTCGCAT GA

42

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAAGGATCCA CCATGCAGCA GCCCTTCAAT T

31

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bas pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTTGGATCCT TAGAGCTTAT ATAAGCCGA

29

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAAGAATTCCG GTACCATGCC GGAGGAGGGT TCGG

34

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TTTGGATCCT CAGGGGCGCA CCCACTGCA

29

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ile	Ser	Gln	Ala	Val	His	Ala	Ala	His	Ala	Glu	Ile	Asn	Glu	Ala	Gly
1				5					10					15	

Arg

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Pro Lys Tyr Val Lys Gln Asn Thr Leu Lys Leu Ala Thr
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Lys Thr Ile Ala Thr Asp Glu Glu Ala Arg Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gln Ala Ser Leu Ala Leu Ser Tyr Arg Leu Asn Met Phe Thr Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: lin ar

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Phe	Val	Arg	Phe	Asp	Ser	Asp	Ala	Ala	Ser	Gln	Arg	Met
1				5						10		